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SEQUENCE LISTING

<110> Xia, Zhi-Qiang
Costa, Michael A
Davin, Laurence B
Lewis, Norman G

<120> Recombinant Secoisolariciresinol Dehydrogenase, and
Methods of Use

<130> WSUR116430

<140> 09/673,918

<141> 2000-10-23

<150> PCT/US99/08975

<151> 1999-04-23

<150> 60/082,977

<151> 1998-04-24

<160> 25

<170> PatentIn Ver. 2.0

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<211> 819

<212> DNA

<213> Forsythia x intermedia

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Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp	Val	Gln	Asp	Glu	
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Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser	Asn	Ser	Thr	Tyr	
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Asn	Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met	Phe	Ser	Asn	Ala	
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gca	gtc	gag	ctc	gga	caa	ttt	ggc	att	agg	gtt	aat	tgt	ttg	tct	cct	576	
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Phe	Gly	Leu	Pro	Thr	Ala	Leu	Gly	Lys	Lys	Phe	Ser	Gly	Ile	Lys	Asn		
		195					200					205					
gaa	gaa	gaa	ttt	gag	aat	gta	ata	aac	ttt	gcg	gga	aat	ttg	aaa	ggg	672	
Glu	Glu	Glu	Phe	Glu	Asn	Val	Ile	Asn	Phe	Ala	Gly	Asn	Leu	Lys	Gly		
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Pro	Lys	Phe	Asn	Val	Glu	Asp	Val	Ala	Asn	Ala	Ala	Leu	Tyr	Leu	Ala		
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Ser	Asp	Glu	Ala	Lys	Tyr	Val	Ser	Gly	His	Asn	Leu	Phe	Ile	Asp	Gly		
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Gly	Phe	Ser	Val	Cys	Asn	Ser	Val	Ile	Lys	Val	Phe	Gln	Tyr	Pro	Asp		
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Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr			
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Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp			
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Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala			
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Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala			
	100	105	110
Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys			
	115	120	125
Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile			
	130	135	140
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His			
145	150	155	160
Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu			
	165	170	175
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro			
	180	185	190
Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn			
	195	200	205
Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly			
	210	215	220
Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala			
225	230	235	240
Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly			
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Ser			

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aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat	35	40	45	144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp				
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc act tcc	50	55	60	192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser				
aat tcc acc tac atc cac tgt gat gtt act aat gaa gac ggt gtt aaa	65	70	75	240
Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys				
aat gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg	85	90	95	288
Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met				
ttc agc aat gca gga att tct gat ccc aac agg ccc cgc atc ata gac	100	105	110	336
Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp				
aac gaa aaa gca gac ttt gaa cgc gtt ttc agt gta aat gta acc gga	115	120	125	384
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly				
gtt ttc cta tgc atg aag cac gca gca cgt gtt atg att cca gca cgc	130	135	140	432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg				
agt ggc aac ata att tcc act gct agt tta agc tca act atg ggt ggt	145	150	155	480
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly				
ggt tct tca cat gcc tat tgt ggt tca aag cat gct gtg tta ggc ctt	165	170	175	528
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu				
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat	180	185	190	576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn				
tgt ttg tct cct ttc ggg ctt cct acg gct tta ggc aag aaa ttt tca	195	200	205	624
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser				
ggg att aaa aat gaa gaa gaa ttt gag aat gta ata aac ttt gcg gga	210	215	220	672
Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly				
aat ctg aaa ggt cca aaa ttt aat gtt gag gat gtt gcc aat gca gct	225	230	235	720
Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala				
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Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe						
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Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp						
	35		40		45	
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser						
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Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys						
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Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met						
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Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp						
	100		105		110	
Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly						
	115		120		125	
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg						
	130		135		140	
Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly						
	145		150		155	160
Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu						
		165		170		175
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn						
	180		185		190	
Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser						
	195		200		205	
Gly Ile Lys Asn Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly						
	210		215		220	
Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala						

225		230		235		240
Leu Tyr Leu Ala Ser	Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu					
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ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca gca aaa ctc	96
Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu	
20 25 30	
ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa	144
Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu	
35 40 45	
tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac	192
Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr	
50 55 60	
atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac	240
Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp	
65 70 75 80	
aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca	288
Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala	
85 90 95	
gga att tct gat ccc tac aag ccc cgg gtc ata gac aac gaa aaa gca	336
Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala	
100 105 110	
gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt	384
Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe	
115 120 125	
atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata	432
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile	
130 135 140	
att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat	480
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His	

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	165	170	175	
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	180	185	190	
ttc ggg ctt cct acg cct cta gcc aag aaa ttt tca ggg att gaa aat	Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn	624		
	195	200	205	
gat gta gac ttt gcg aat gca ata gaa cat gcg gga aat ctg aaa ggt	Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly	672		
	210	215	220	
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	225	230	235	240
agt gat gag gca caa tat gtg agt gga caa aat ctg ttc atc gat gga	Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly	768		
	245	250	255	
ggg ttc agc gtc tgc aat tct gca atc aaa atg ttc caa tat cca gac	Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp	816		
	260	265	270	
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Ser				

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 35 40 45
 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr
 50 55 60
 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp
 65 70 75 80
 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala
 85 90 95
 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala
 100 105 110

Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe
115 120 125
Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile
130 135 140
Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His
145 150 155 160
Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu
165 170 175
Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro
180 185 190
Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn
195 200 205
Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly
210 215 220
Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala
225 230 235 240
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Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp
260 265 270

Ser

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Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe
20 25 30
aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat 144
Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp
35 40 45
gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc atc ggc act tcc 192
Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser
50 55 60

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Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys	
65 70 75 80	
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Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met	
85 90 95	
ttc aac aat gca gga att gct gac ccc aac aag ccc cgc atc gta gac	336
Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp	
100 105 110	
aac gaa aaa gca gac ttt gaa cgc gtt ctc agc gta aat gta acc ggt	384
Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly	
115 120 125	
gtt ttc cta tgc atg aag cac gca gca cgc gtt atg gtg cca gca cgc	432
Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg	
130 135 140	
agt ggc agc ata att tcc act gct agc gta agc tca aca att ggt ggt	480
Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly	
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gct gct tca cat gct tat tgt tgt tca aag cat gct gtg tta ggc ctt	528
Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu	
165 170 175	
act agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat	576
Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn	
180 185 190	
tgt ttg gct cct tac gcg ctt gct acg cct tta gcc aag aaa ttt gta	624
Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val	
195 200 205	
ggg ctt gaa aat gac gaa gat ttg gag aat gca atg agc ctt atg gga	672
Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly	
210 215 220	
aat ctg aaa ggt aca aat ttg aag gct gag gac gtc gcc aat gca gct	720
Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala	
225 230 235 240	
ctt tat ctg gca agt gat gag gca aaa tat gtg agt gga cac aat ctg	768
Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu	
245 250 255	
ttc att gat gga ggg ttc agc gtc tac aat tct gca atc aaa atg ttc	816
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260 265 270	
caa tat cca gac act	831
Gln Tyr Pro Asp Thr	
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<213> Forsythia x intermedia

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			20					25					30		
Thr	Ala	Lys	Leu	Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp
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Val	Gln	Asp	Glu	Leu	Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser
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Asn	Ser	Ile	Tyr	Ile	His	Cys	Asp	Val	Thr	Asn	Glu	Asp	Asp	Val	Lys
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Phe	Asn	Asn	Ala	Gly	Ile	Ala	Asp	Pro	Asn	Lys	Pro	Arg	Ile	Val	Asp
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Asn	Glu	Lys	Ala	Asp	Phe	Glu	Arg	Val	Leu	Ser	Val	Asn	Val	Thr	Gly
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Val	Phe	Leu	Cys	Met	Lys	His	Ala	Ala	Arg	Val	Met	Val	Pro	Ala	Arg
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Ser	Gly	Ser	Ile	Ile	Ser	Thr	Ala	Ser	Val	Ser	Ser	Thr	Ile	Gly	Gly
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Ala	Ala	Ser	His	Ala	Tyr	Cys	Cys	Ser	Lys	His	Ala	Val	Leu	Gly	Leu
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Thr	Arg	Asn	Leu	Ala	Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn
			180					185					190		
Cys	Leu	Ala	Pro	Tyr	Ala	Leu	Ala	Thr	Pro	Leu	Ala	Lys	Lys	Phe	Val
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Gly	Leu	Glu	Asn	Asp	Glu	Asp	Leu	Glu	Asn	Ala	Met	Ser	Leu	Met	Gly
	210					215					220				
Asn	Leu	Lys	Gly	Thr	Asn	Leu	Lys	Ala	Glu	Asp	Val	Ala	Asn	Ala	Ala
225					230					235				240	
Leu	Tyr	Leu	Ala	Ser	Asp	Glu	Ala	Lys	Tyr	Val	Ser	Gly	His	Asn	Leu
				245					250					255	
Phe	Ile	Asp	Gly	Gly	Phe	Ser	Val	Tyr	Asn	Ser	Ala	Ile	Lys	Met	Phe
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 <222> (1)..(828)

<400> 9
 atg gcc act tca cag ctt cga act gca ttc gca aga agg cta gaa gga 48
 Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
 1 5 10 15
 aaa gtt gcc ctt ata aca gga gga gcc agt gga gtt gga gaa gtc aca 96
 Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
 20 25 30
 gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc 144
 Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
 35 40 45
 caa gat gaa tta ggt cac tca gtt gtc gag gcc att ggc ctt tcc aat 192
 Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
 50 55 60
 tcc acc tac atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat 240
 Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65 70 75 80
 gcc gtg gac aac aca gtt tca acc tat gga aaa ctg gac att atg ttc 288
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
 85 90 95
 aac aat gca gga att tct gat ccc tac aag ccc cgg gtc ata gac aac 336
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
 100 105 110
 gaa aaa gca gac ttt gaa cgc gtt ctc agt gtt aat gta acc gga gtt 384
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
 115 120 125
 ttc cta ttt atg aag cac gca gca cgc att atg gtt cca gca cga agt 432
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
 130 135 140
 ggc tgc ata att tcc act gct agt tta agc tca act atg ggt ggt ggt 480
 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
 145 150 155 160
 tct tca cat gct tat tgt ggt tca aag cat gct gta tta ggc ctt act 528
 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
 165 170 175
 agg aat ctg gca gtc gag ctc gga caa ttt ggc att agg gtt aat tgt 576
 Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
 180 185 190
 ttg tct cct ttc ggg ctt cct acg cct tta gcc aag aaa ttt aca ggg 624
 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
 195 200 205

att gaa aat gat gaa gac ttg gcg aat gga ata gaa cgt gcg gga aat	672
Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn	
210 215 220	
ctg aaa ggt aca aaa ttg agg att gag gat gtt gcc aat gca gct ctt	720
Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu	
225 230 235 240	
ttt ctg gct agt gat gag gca caa tat gtg agt gga caa aat ctg ttc	768
Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe	
245 250 255	
atc gat gga ggg ttc agc gtc tgc aat tct gca atc aaa ttg ttc caa	816
Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln	
260 265 270	
tat cca gac tct	828
Tyr Pro Asp Ser	
275	

<210> 10
 <211> 276
 <212> PRT
 <213> Forsythia x intermedia

<400> 10
 Met Ala Thr Ser Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly
 1 5 10 15
 Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr
 20 25 30
 Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val
 35 40 45
 Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Leu Ser Asn
 50 55 60
 Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn
 65 70 75 80
 Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe
 85 90 95
 Asn Asn Ala Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn
 100 105 110
 Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val
 115 120 125
 Phe Leu Phe Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Ser
 130 135 140
 Gly Cys Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly
 145 150 155 160
 Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr
 165 170 175

Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys
180 185 190

Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly
195 200 205

Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn
210 215 220

Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu
225 230 235 240

Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe
245 250 255

Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln
260 265 270

Tyr Pro Asp Ser
275

<210> 11
<211> 21
<212> PRT
<213> Forsythia x intermedia

<220>
<221> PEPTIDE
<222> (1)..(21)
<223> N-terminal peptide of F. intermedia
secoisolariciresinol protein wherein Xaa at
positions 3, 12 and 20 represents an unidentified
amino acid residue

<400> 11
Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu
1 5 10 15

Ile Thr Gly Xaa Ala
20

<210> 12
<211> 17
<212> PRT
<213> Forsythia x intermedia

<400> 12
Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala
1 5 10 15

Lys

<210> 13
<211> 15
<212> PRT

<213> Forsythia x intermedia

<400> 13

Leu Asn Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Lys
1 5 10 15

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> PCR primer wherein n at positions 3, 9, 15 and 18
represents inosine

<400> 14

ggnathggng aracnacngc

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 15

ccngcrttng araacatdat

20

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>

<221> misc_feature

<222> (1)..(20)

<223> PCR primer wherein n at positions 3 and 9
represents inosine

<400> 16
ccngcrttnc traacatdat 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer

<400> 17
attccgctag attgcattga 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3 and 9
represent inosine

<400> 18
ccngcrttnc traacatdat 20

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(20)
<223> T7 PCR primer

<400> 19
aattaaccct cactaaaggg 20

<210> 20

<211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
 <221> misc_feature
 <222> (1)..(23)
 <223> PCR primer

<400> 20
 cagcttcgaa ctgcattcgc aag 23

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
 <221> misc_feature
 <222> (1)..(22)
 <223> T7 PCR primer

<400> 21
 cgggatatca ctcagcataa tg 22

<210> 22
 <211> 816
 <212> DNA
 <213> Forsythia x intermedia

<220>
 <221> CDS
 <222> (1)..(816)

<400> 22
 cag ctt cga act gca ttc gca aga agg cta gaa gga aaa gtt gcc ctt 48
 Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu
 1 5 10 15
 ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc 96
 Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
 20 25 30
 tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta 144
 Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
 35 40 45
 ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc 192
 Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
 50 55 60

cac	tgt	gat	gtt	act	aat	gaa	gac	ggg	gtt	aaa	aat	gcc	gtg	gac	aac	240
His	Cys	Asp	Val	Thr	Asn	Glu	Asp	Gly	Val	Lys	Asn	Ala	Val	Asp	Asn	
65					70					75					80	
aca	gtt	tca	acc	tat	gga	aaa	ctg	gac	att	atg	ttc	agc	aat	gca	gga	288
Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met	Phe	Ser	Asn	Ala	Gly	
				85					90					95		
att	tct	gat	ccc	aac	agg	ccc	cgc	atc	ata	gac	aac	gaa	aaa	gca	gac	336
Ile	Ser	Asp	Pro	Asn	Arg	Pro	Arg	Ile	Ile	Asp	Asn	Glu	Lys	Ala	Asp	
			100					105					110			
ttt	gaa	cgc	gtt	ctc	agt	gta	aat	gta	acc	gga	gtt	ttc	cta	tgc	atg	384
Phe	Glu	Arg	Val	Leu	Ser	Val	Asn	Val	Thr	Gly	Val	Phe	Leu	Cys	Met	
		115					120					125				
aag	cac	gca	gca	cgt	gtt	atg	att	cca	gca	cgc	agt	ggc	aac	ata	att	432
Lys	His	Ala	Ala	Arg	Val	Met	Ile	Pro	Ala	Arg	Ser	Gly	Asn	Ile	Ile	
		130				135					140					
tcc	act	gct	agt	tta	agc	tca	act	atg	ggg	ggg	ggg	tct	tca	cat	gcc	480
Ser	Thr	Ala	Ser	Leu	Ser	Ser	Thr	Met	Gly	Gly	Gly	Ser	Ser	His	Ala	
145					150					155					160	
tat	tgt	ggg	tca	aag	cat	gct	gtg	tta	gcc	ctt	act	agg	aat	ctg	gca	528
Tyr	Cys	Gly	Ser	Lys	His	Ala	Val	Leu	Ala	Leu	Thr	Arg	Asn	Leu	Ala	
				165				170						175		
gtc	gag	ctc	gga	caa	ttt	ggc	att	agg	gtt	aat	tgt	ttg	tct	cct	ttc	576
Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn	Cys	Leu	Ser	Pro	Phe	
			180					185					190			
ggg	ctt	cct	acg	gct	tta	ggc	aag	aaa	ttt	tca	ggg	att	aaa	aat	gaa	624
Gly	Leu	Pro	Thr	Ala	Leu	Gly	Lys	Lys	Phe	Ser	Gly	Ile	Lys	Asn	Glu	
		195					200					205				
gaa	gaa	ttt	gag	aat	gta	ata	aac	ttt	gcg	gga	aat	ttg	aaa	ggg	cca	672
Glu	Glu	Phe	Glu	Asn	Val	Ile	Asn	Phe	Ala	Gly	Asn	Leu	Lys	Gly	Pro	
		210				215					220					
aaa	ttt	aat	gtt	gag	gat	gtt	gcc	aat	gca	gct	ctt	tat	ctg	gct	agt	720
Lys	Phe	Asn	Val	Glu	Asp	Val	Ala	Asn	Ala	Ala	Leu	Tyr	Leu	Ala	Ser	
225					230				235						240	
gat	gag	gca	aaa	tac	gtg	agt	gga	cac	aat	ctg	ttc	att	gat	gga	ggg	768
Asp	Glu	Ala	Lys	Tyr	Val	Ser	Gly	His	Asn	Leu	Phe	Ile	Asp	Gly	Gly	
				245				250						255		
ttc	agc	gtc	tgc	aat	tct	gta	atc	aaa	gtg	ttc	caa	tat	cca	gat	tct	816
Phe	Ser	Val	Cys	Asn	Ser	Val	Ile	Lys	Val	Phe	Gln	Tyr	Pro	Asp	Ser	
			260					265					270			

<210> 23

<211> 272

<212> PRT

<213> Forsythia x intermedia

<400> 23

Gln	Leu	Arg	Thr	Ala	Phe	Ala	Arg	Arg	Leu	Glu	Gly	Lys	Val	Ala	Leu
1				5					10					15	
Ile	Thr	Gly	Gly	Ala	Ser	Gly	Ile	Gly	Glu	Thr	Thr	Ala	Lys	Leu	Phe
		20						25					30		
Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp	Val	Gln	Asp	Glu	Leu
		35					40					45			
Gly	His	Ser	Val	Val	Glu	Ala	Ile	Gly	Thr	Ser	Asn	Ser	Thr	Tyr	Ile
	50					55					60				
His	Cys	Asp	Val	Thr	Asn	Glu	Asp	Gly	Val	Lys	Asn	Ala	Val	Asp	Asn
65					70					75					80
Thr	Val	Ser	Thr	Tyr	Gly	Lys	Leu	Asp	Ile	Met	Phe	Ser	Asn	Ala	Gly
				85					90					95	
Ile	Ser	Asp	Pro	Asn	Arg	Pro	Arg	Ile	Ile	Asp	Asn	Glu	Lys	Ala	Asp
			100					105					110		
Phe	Glu	Arg	Val	Leu	Ser	Val	Asn	Val	Thr	Gly	Val	Phe	Leu	Cys	Met
		115					120					125			
Lys	His	Ala	Ala	Arg	Val	Met	Ile	Pro	Ala	Arg	Ser	Gly	Asn	Ile	Ile
	130					135					140				
Ser	Thr	Ala	Ser	Leu	Ser	Ser	Thr	Met	Gly	Gly	Gly	Ser	Ser	His	Ala
145					150					155					160
Tyr	Cys	Gly	Ser	Lys	His	Ala	Val	Leu	Ala	Leu	Thr	Arg	Asn	Leu	Ala
				165					170					175	
Val	Glu	Leu	Gly	Gln	Phe	Gly	Ile	Arg	Val	Asn	Cys	Leu	Ser	Pro	Phe
			180					185					190		
Gly	Leu	Pro	Thr	Ala	Leu	Gly	Lys	Lys	Phe	Ser	Gly	Ile	Lys	Asn	Glu
		195					200					205			
Glu	Glu	Phe	Glu	Asn	Val	Ile	Asn	Phe	Ala	Gly	Asn	Leu	Lys	Gly	Pro
	210					215					220				
Lys	Phe	Asn	Val	Glu	Asp	Val	Ala	Asn	Ala	Ala	Leu	Tyr	Leu	Ala	Ser
225					230					235					240
Asp	Glu	Ala	Lys	Tyr	Val	Ser	Gly	His	Asn	Leu	Phe	Ile	Asp	Gly	Gly
				245					250					255	
Phe	Ser	Val	Cys	Asn	Ser	Val	Ile	Lys	Val	Phe	Gln	Tyr	Pro	Asp	Ser
			260					265					270		

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 24
acatatgcag cttcgaactg cattcgcaag aag

33

<210> 25
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(33)
<223> PCR primer

<400> 25
catatgggca gacatgttac atgatcaatt gca

33